SEQUENCE LISTING

<110> Banerjee, Subhashis
Taylor, Lori K
Spiegler, Clive E
Tracey, Daniel E
Chartash, Elliot K
Hoffman, Rebecca S
Barchuk, William T
Yan, Philip
Murtaza, Anwar
Salfeld, Jochen G
Fischkoff, Steven

<120> TREATMENT OF TNFα RELATED DISORDERS

<130> BPI-187

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<150> 60/397,275
<151> 2002-07-19

<150> 60/411,081
<151> 2002-09-16

<150> 60/417,490
<151> 2002-10-10

<150> 60/455,777
<151> 2003-03-18

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Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Arg	Asn	Tyr
			20					25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Ala	Ala	Ser	Thr	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80
Glu	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	Gln	Arg	Tyr	Asn	Arg	Ala	Pro	Tyr
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Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys					

100 105

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1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
50 55 60
Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<220>
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<223> Xaa = Thr or Ala

<223> Mutated human antibody

<400> 3
Gln Arg Tyr Asn Arg Ala Pro Tyr Xaa
1 5

<210> 4
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<220>
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<223> Mutated human antibody

<400> 4

Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Xaa
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Ala Ala Ser Thr Leu Gln Ser
1 5

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<400> 6
Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu
1 5 10 15
Gly

<210> 7
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<400> 7
Arg Ala Ser Gln Gly Ile Arg Asn Tyr Leu Ala
1 5 10

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<400> 8
Asp Tyr Ala Met His
1 5

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Tyr
                85                  90                  95
Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Val
        35                  40                  45
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
    50                  55                  60
Glu Gly Arg Phe Ala Val Ser Arg Asp Asn Ala Lys Asn Ala Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Thr Lys Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu Asp Asn Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser
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Gln Lys Tyr Asn Ser Ala Pro Tyr Ala
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<400> 12
Gln Lys Tyr Asn Arg Ala Pro Tyr Ala
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Gln Lys Tyr Gln Arg Ala Pro Tyr Thr
1 5

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Gln Lys Tyr Ser Ser Ala Pro Tyr Thr
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Gln Lys Tyr Asn Arg Ala Pro Tyr Thr
1 5

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<400> 17
Gln Lys Tyr Asn Ser Ala Pro Tyr Tyr
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<220>
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<400> 18
Gln Lys Tyr Asn Ser Ala Pro Tyr Asn
1 5

<210> 19
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<400> 19
Gln Lys Tyr Thr Ser Ala Pro Tyr Thr
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Gln Lys Tyr Asn Arg Ala Pro Tyr Asn
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<400> 21
Gln Lys Tyr Asn Ser Ala Ala Tyr Ser
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<400> 22
Gln Gln Tyr Asn Ser Ala Pro Asp Thr
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<400> 23
Gln Lys Tyr Asn Ser Asp Pro Tyr Thr
1 5

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<400> 24
Gln Lys Tyr Ile Ser Ala Pro Tyr Thr
1 5

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<400> 25
Gln Lys Tyr Asn Arg Pro Pro Tyr Thr
1 5

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<400> 30

Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu Asp Asp
1 5 10

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1 5 10

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<400> 33
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<400> 34
Ala Ser Tyr Leu Ser Thr Ala Ser Ser Leu Glu Tyr
1 5 10

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<400> 35
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 1   5   10

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gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaatcagg ggtcccatct 180
cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctacagcct 240
gaagatgttg caacttatta ctgtcaaagg tataaccgtg caccgtatac ttttggccag 300
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ccagggaagg gcctggaatg ggtctcagct atcacttgga atagtggtca catagactat 180
gcggactctg tggagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggat acggccgtat attactgtgc gaaagtctcg 300
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agt   363